

Fig. 1A

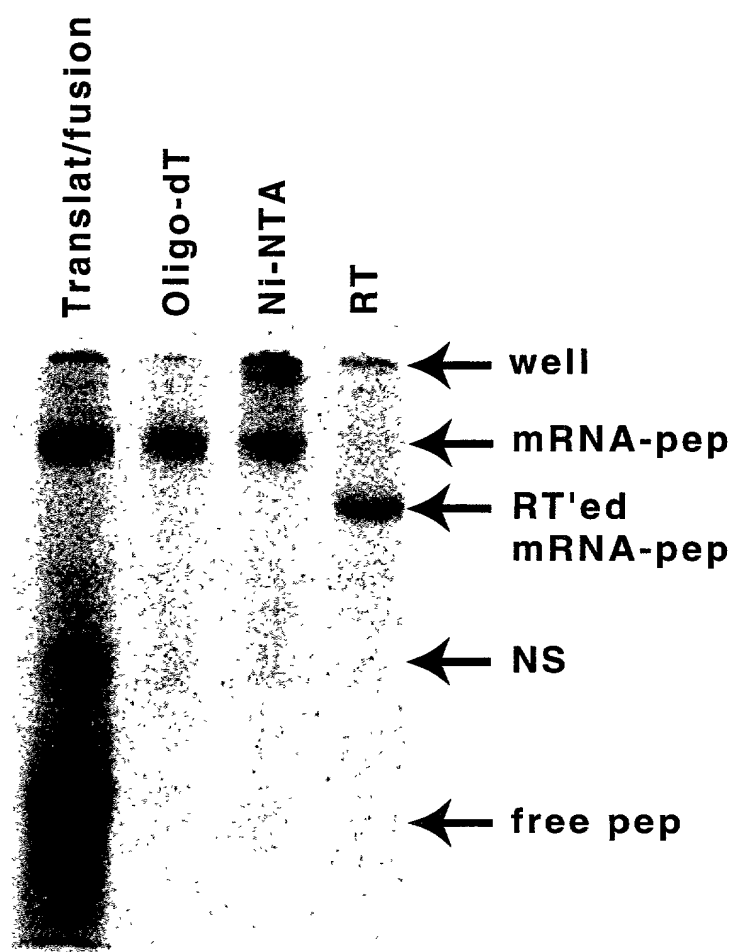


Fig. 1B

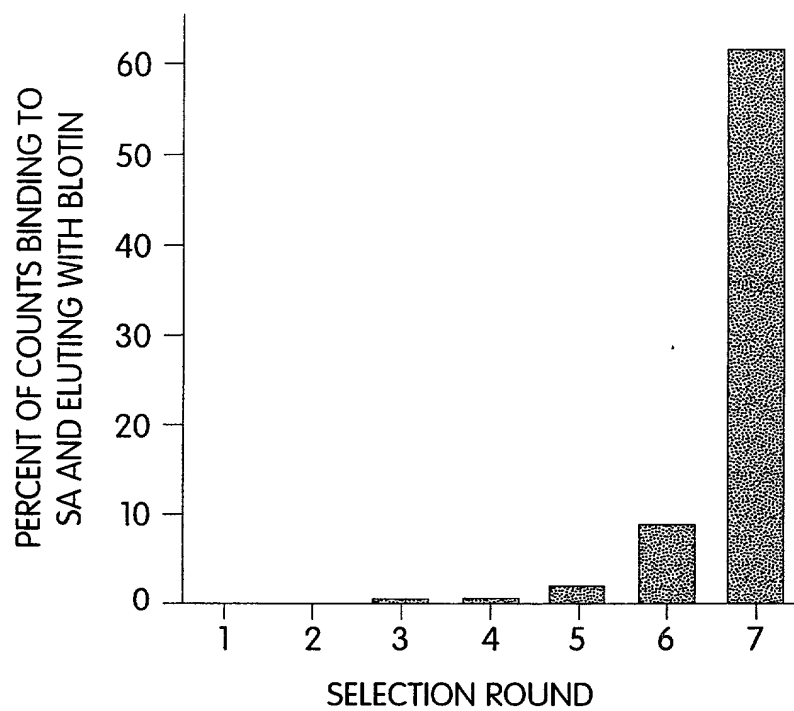


Fig. 2A

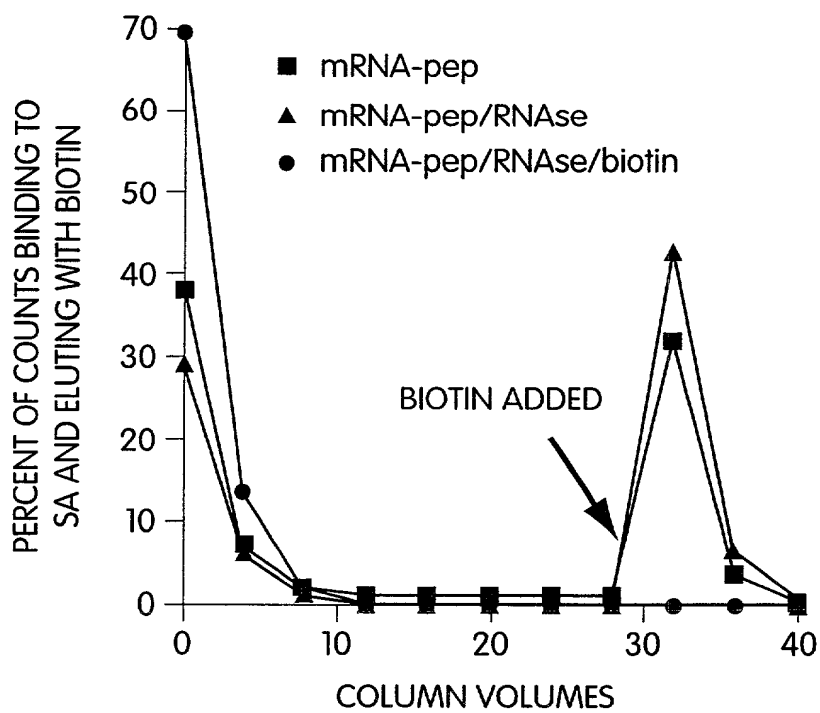


Fig. 2B

name #	SEQ ID NO:
SB1 3	<u>MDEKTHCTIS</u> MNGAVPLVPHH HPQ GDPLRLLRPQPALLVVR HPQ GDVLVALVEHHEGVDRGLVALPELHAEEELGEPVGDIVQGPVEQVQGVWDALVWRLPPS 1
SB2 2	<u>MDEKTHCFHP</u> GDHLVRLVEELQALAEGLRQCGRQPHRLPRRRPHHLQLLLDEA HPQ AGPLRERAHQVDGRLLQLQH HPQ GDRLLQQPDQHPLELVWRLPPS 2
SB3 4	<u>MTRRPTASS</u> SSCVRHLLLRQGEHGHQALEDRDKARHVRLVEGDVEVLGGDLRLARARHEAL HPQ AGLVHLPLHGGDLGGHLRLVLEA HPQ GDRLLGLAVHHH 3
SB4 1	<u>MDEKTHWGIS</u> TWRGEPLLH HPQ AGRLPLDRRRARHRLILGAEPGGVDHGILLELLDDHRPLVPD HPQ RGPLQRGDLPQVVPVLRHAHVGLGLAAATIT 4
SB5 3	<u>MDEKTHWNVVY</u> HPQ GDLLVRGHGHVREALHDQGLHQDLLVGPPEVVVRALRGVEVLGGRLRLVPL HPQ GEALDQARQRPQHLLLELHHRALPPALVWRLPPS 5
SB6 1	<u>MDEKTHWLN</u> NFEEELARLDGLREGEDHPLVLRH HPQ GDGLLDQPLGRHRAIDGEVREGDRPLDQGGEDLGALVDDDEVLDCGLVHVGVHVDPLVCGCHHH 6
SB7 1	<u>MDEKTHWFG</u> TLSFPTHMSAVNGKIDCSFNMLSSGHPDGDALDDQ HPQ GDALVGRDDGVQALRLEGHQHRRLAQRRADRHRQLVWRLPPS 7
SB8 1	<u>MDEKTHCTI</u> ELNFSFTHMKLHH HPQ GDALLDDGVRPHPLADEGGGLDQGLCHRRGVVAERLARRDPEVLEGLVERHRLVPRLRHGGERHAEPVWRLPPS 8
SB9 1	<u>MDEKTHCNT</u> GLYDGAADCFNELNKDVAPLVEGRHDLVEGLLLER HPQ GDPLVAHRQLVHHPLLGRGERHRRALVPQQEHQPHRLQPVVDLGRRLVWRLPPS 9
SB10 1	<u>MDEKTHWHER</u> AQELVGGILLHD HPQ RRLLLEPRGPRPLRGLVHERGHQPPLAGRVEEADGGLLRDGGGELEPLVREGEDHLEPLDDELDAQPRGLVWRLPHHH 10
SB11 1	<u>MDEKTHWHER</u> VHHLADGLEQ HPQ GQRRPLVERHRQVPRGLVRELQHEGLPLEHPAGVHVIRLHQGDDRDVDGLVDGHRDVRGLEREVGDPHRLVWRLPPS 11
SB12 4	<u>MDKPLLEE</u> LEELRERLVH HPQ GGILLPLRGQVGHDAFRIGAEDVDLGGLLDEPQRAVAGLHHVPHRVGQRLVHEVRELDEGLLDQRDDLRQRLVWRLPPS 12
SB13 2	<u>MEREDPL</u> DEQLRELREALVD HPQ GGAQALHRHDGGHVPLRRVQHRLOPGLQHHLPEQPPLGGLQELQARLQPLAGEHEGDGAGLQRPVGHQGRRLVWRLPPS 13
SB14 1	<u>MDEKTHRT</u> LSVLSFNWLQTKACWRLVEGLHG HPQ GLVREHEVDVPLAEFVQQVWGLADGVEQPGGGLLHRAQRVDHPLPDHAGQVLGRVWRLPPS 14
SB15 1	<u>MDEKTHW</u> LEDLKGVLKDCLKDLMDFTKDCRSRVQPPQLLHHRGEPVPLLREAGRDLGGLPRAPRQARPLHGRHDLHEPLVLQD HPQ GGPLVCGCHHH 15
SB16 1	<u>MDEKTHW</u> VLQ HPQ GDRLGPRHGGDDVRLVGQGEGLVLEGLDGRPRRRRRLPREDEHRVRALVDQVRDLAERLVEEVDGGVEALRHLGLPQDEPRSGGCHHH 16
SB17 2	<u>MDEKTHW</u> VDLQEPPLGPHGGVGEVPGGLVLRH HPQ DRDLVDGVGPHGRALARRPHRVVEGLHLLLRGGERLPPDGPRQLGLLGGELDRADPALVWRLPPS 17
SB18 1	<u>MDEKTHCA</u> VNVNVLTHWCHRV AHLQPLD HPQ GDHLRLEPLGHALVDPLVQGVVEEVRPLQLDVGVRVALVEQVAEVGEGLDHEAGQAAGALVWRLPPS 18
SB19 1	<u>MDEKTTG</u> WRGGHVVEGLAGELEQLRARLEH HPQ GQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVEKLLTDWFKFNVSCKDKMTFYLEMYDMSGGCHHH 19
SB20 1	<u>MNEKTHCK</u> LNFKVNIADWLAEFHGGGGLLGRRDGVVQRLVDGVQERVERLDRDPGLGLRLLELHHRDHRLRLGGEHLRLDHPLEPDDHLVVGGLVWRLPPS 20

Fig. 3

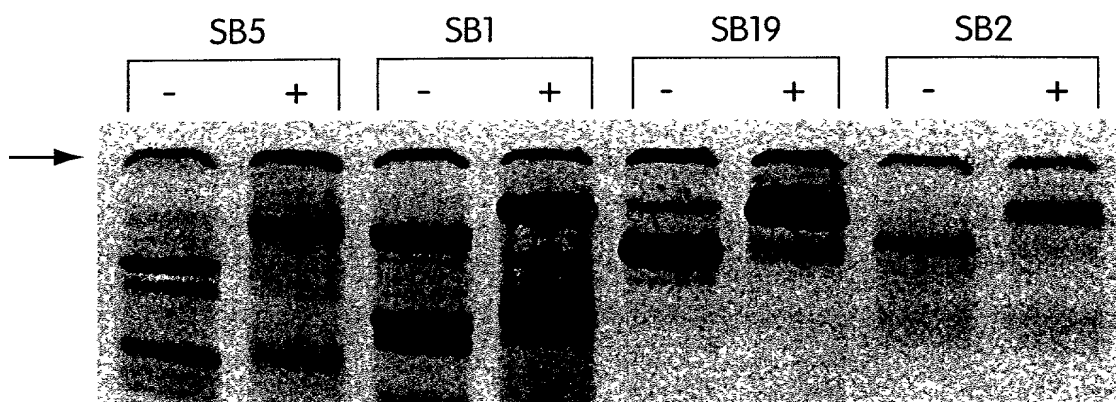


Fig. 4A

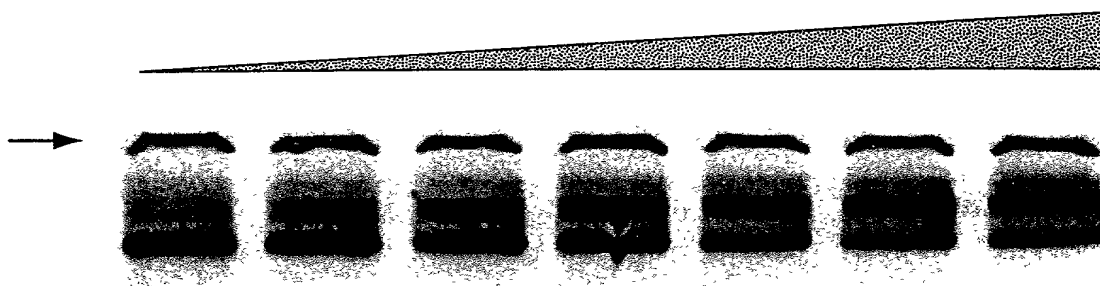


Fig. 4B

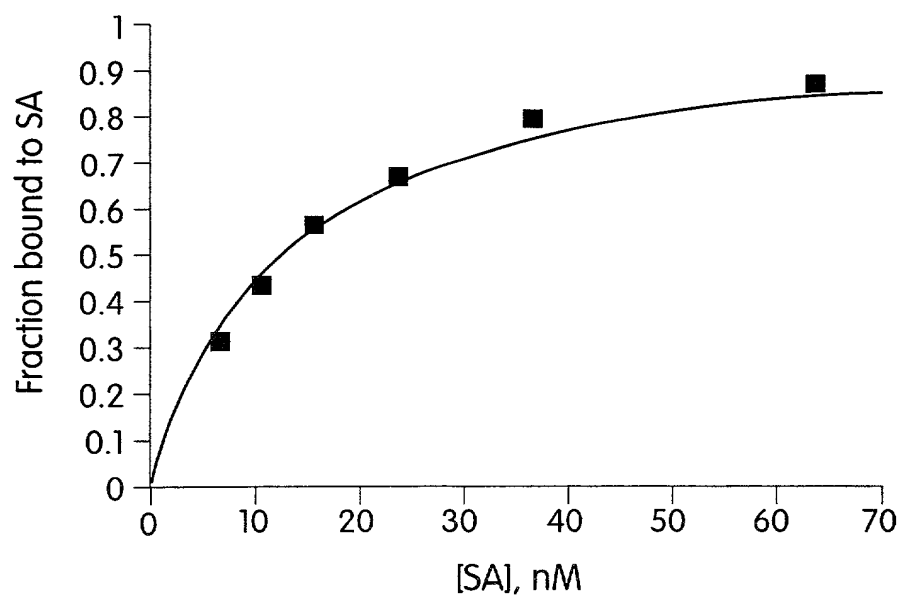


Fig. 4C

		% binding	SEQ ID NO:
FL	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVEKLLTDWFKFKNVSKDCKMTFYLEMYSGGCKLG	85	21
C1	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVEKLLTDWFKFKNV	87	22
C2	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVE	88	23
C3	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVE	89	24
C4	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQ	88	25
M1	MDEKTTGWRGGHVVEGLAGELEQLRARLEHHPQGGQREPLVQEVEDVDEGLVQDLHGVAAGLLDPVE	0.065	26
N1	MD	69	27
N2	MD	30	28
N3	M	0.058	29

Fig. 5

CGCAAAATTGTGCGGCGGATTAAATCTCGCGCGGATCAACTGGTGCCAGCGTGGTGTGATGGTAGAACGAAGCGGC
 GTCGAAGCCTGTAAAGCGGCGGTGCACAAATCTTCTCGCGCAACGCGTCAGTGGGTGATCATTAACATATCCGCTGGATGA
 CCAGGATGCCATTGCTGTGGAAGCTGCCGTGCATAATGTTCCGGCGTTATTTCTTGATGTCTTGACCAGACACCCCATCA
 ACAGTATTATTTCTCCCATGAAGACGGTACCGGACTGGCGTGGAGCATCTGGTCGCATTGGGTACCCAGCAAAATCGCG
 CTGTTAGCGGCGCCATTAAATTCTGTCTCGCGCGCTGCGTCTGGCTGGCTGGCATAAATATCTACTCGCAATCAAAAT
 TCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTCAACAAACCATGCAAAATGCTGAATGAGGGCA
 TCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGCGC
 GTTGGTGGGATATCTCGGTAGTGGGATACGAGATACCGAAGACAGCTCATGTTATATCCCGCGTTAACCCATCAA
 ACAGGATTTTCGCTGCTGGGCAACACAGCGTGACCGCTTGCTGCAACTCTCAGGGCCAGGCGGTGAAGGCAATC
 AGCTGTTGCCCGTCTCACTGGTGAAAGAAACCAACCTGGCGCCCAATACGAAACCGCTCTCCCCGCGTTGGCC
 GATTCAATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAGCGGCGAGTGAGCGCAACGCAATTAATGTAAGTTAGC
 TCACTCATTAGGCACCGGATCTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGCGCGGGGC
 ATGACTATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGCGCAGCGCTCTGGGTCA
 TTTCGGCGAGGACCGCTTTCGCTGGAGCGGACGATGATCGGCTGTGCTTGGGTATTCGGAATCTTGACGCCCCTCG
 CTCAAGCCTTCGTCACTGGTCCCGCCCAACAAAGTTTCGGGAGAGCAGGCCATTATCGCGGCATGGCGGCCACCG
 GTGCGCATGATCGTGTCTGTTGAGACCCCGTAGGCTGGCGGGTTCCTTACTGTTAGCAGAAATGAATCAACC
 GATACGCGAGCGAACGTGAAGCACTGTCTGCAAAACGTCTGCGACCTGAGCAACAACATGAATGGTCTTCGGTTTCC
 GTGTTTCGTAAAGTCTGGAAACCGGGAAGTCAGGCCCCTGACCATTATGTTCCGGATCTGCATCGCAGGATGCTGCTGG
 CTACCCGTGTGGAACACCTACATCTGTATTAAACGAAGCGCTGGCATTTGACCTGAGTGATTTTCTCTGGTCCCGCGCAT
 CCATACCGCCAGTTGTTTACCCCTCAACACGTTCCAGTAACCGGGCATGTTTCATCATCAGTAACCCGATCTCGTGAGCATCC
 TCTCTCGTTTCATCGGTATCATTAACCCCATGAACAGAAATCCCCCTTACACGGAGGCATCAGTGACCAACAGGAAAAA
 ACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTACGCTTCTGGAGAAACTCAACGAGCTGGACGCGGATGA
 ACAGGCAGACATCTGTGAATCGCTTCACGACCCACGCTGATGAGCTTTACCGCAGCTGCCCTCGCGCTTTCGGTGATGACG
 GTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGCTGTAAAGCGGATGCCGGGAGCAGACAAGCCCCGT
 CAGGGCGGCTCAGCGGTGTGGCGGTGTCCGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGG
 CTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCAACCATATATGCGGTGTGAAATACCGCACAGATGCGTAAGG
 AGAAAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGGTTCGGTTCGGCGAGCGGT
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 AGCAAAAGGCCAGGAACCGTAAAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCTTACGAGCATCACAAA
 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCCCTGGAAGCTCCCTCGT
 GCGCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTCTCTCCCTTCGGGAAGCGTGGCGCTTCTCATATA

Fig. 6A (continued)

GCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTCAAGCTGGCTGTGTGCACGAACCCCCCGTTAGCCCC
 GACCGTGGCCCTTATCCGGTAACATACTGCTTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC
 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA
 GAAGACAGTATTGGTATCTGCGCTCTGCTGAAGCAGTTACCTTCGGAAAAAGAGTTGGTAGTCTTTGATCCGGCAAA
 CAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATTACGGCAGAAAAAAGGATCTCAAGAAGATCC
 TTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGATTTTGGTCATGAACAATAAAACTG
 TCTGCTTACATAAACAGTAATAACAAGGGGTGTTATGAGCCATATTCAACGGGAAACGCTTGTCTTAGGCCGGATTAAA
 TTCCAACATGGATGCTGATTATATGGGTATAAATGGGCTCGGATAATGTGGGCAATCAGGTGCGACAATCTATCGAT
 TGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATGGCAAGGTAGCGTTGCCAATGATGTTACAGATGAGATG
 GTCAGACTAACTGGCTGACGGAAATTATGCTCTTCCGACCATCAAGCATTTTATCCGTACTCCTGATGATGATGGTT
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 GCTCAGGCGCAATCACGAATGAATAACGGTTTGGTTGATGCGAGTGATTTTGTATGACGAGCGTAATGGCTGGCCGTGTTGA
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 ACCTTATTTTGACGAGGGGAAATTAATAGTTGTATTGATGTTGGACGAGTCGGAATCGCAGACCGATACCCAGGATCTT
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 TGATATGAATAAATTGCAGTTTCAATTGATGCTCGATGAGTTTCTAAGAAATTAATTCATGAGCGGATACATATTTGAA
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 TTTGTTAAAAATTCGCGTTAAATTTTGTAAATCAGCTCATTTTAAACCAATAGGCCGAAATCGGCAAAATCCCTTATA
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 AACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCATAATCAAGTTTTTGGGGTC
 GAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGAGCCCCGATTTAGAGCTTGACGGGGAAGCCGGCGAACGTGG
 CGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGCGCTAGGGCGTGGCAAGTGTAGCGGTCAAGTGGCGGTAAACACC
 ACACCGCGCGCTTAATGCGCGCGCTACAGGGCGGTCCCATTCGCCA

Fig. 6A (continued)

(SEQ ID No.:38)

MGIEEGKLVINGDKGYNGLAENVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEI
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LIAADGGYAFKYENGKYDIKDVGVNAGAKAGLTFLVDLIKKNHNMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSK
VNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYYEELAKDPRIAA
TMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSGSGSGMDEKTTGWRGGHVVEGLAGELEQ
LRARLEHHPQGREPGSGHHHHHHEFLVPRGSMDDPCVKCKVAPRNWKVKNKHLRIYNMCKTCFNNSIDIGDDTYHGHDD

Fig. 6B

(SEQ ID No.:39)

MDPCVKCKVAPRNWKVKNKHLRIYNMCKTCFNNSIDIGDDTYHGHDD

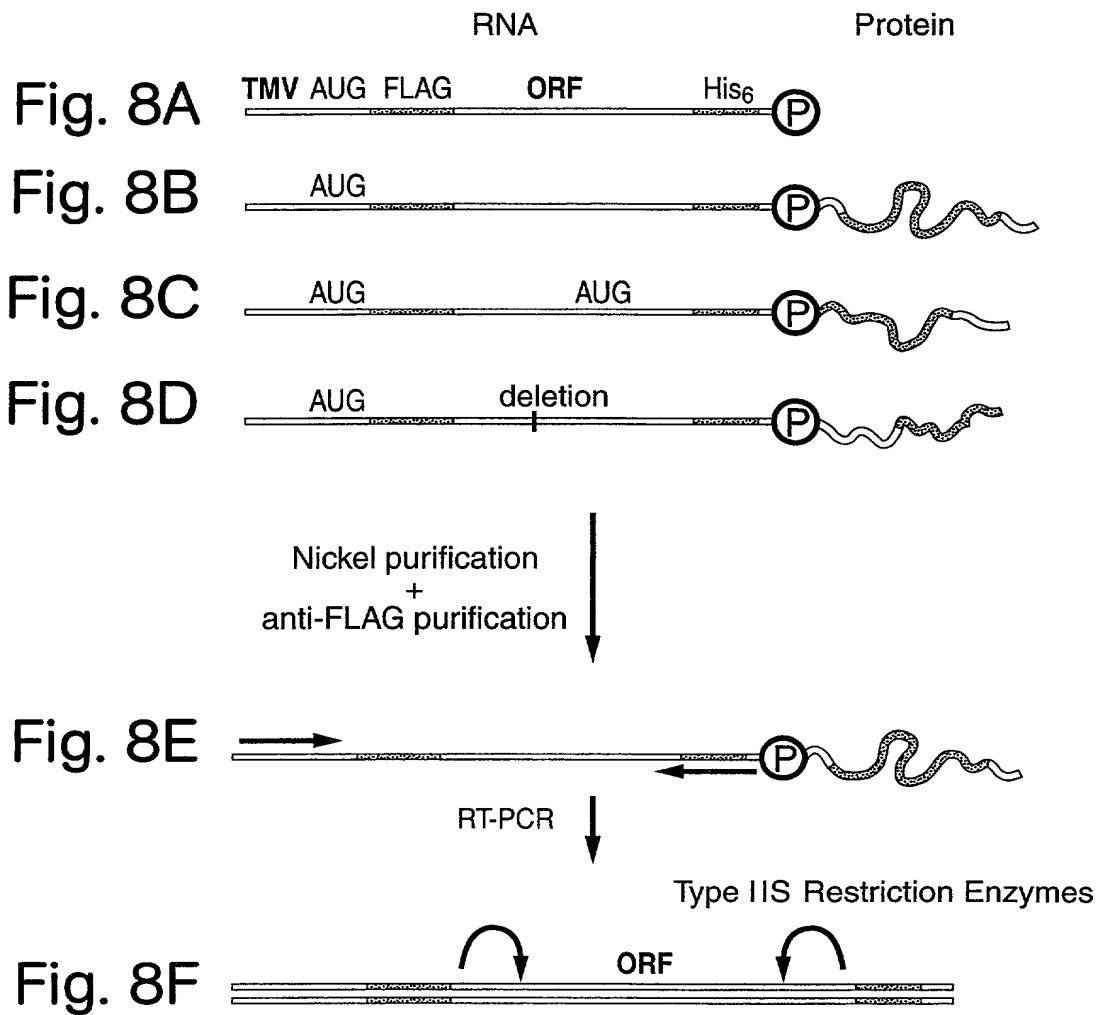
Fig. 6C



Fig. 7A



Fig. 7B



ACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCCACTAATGTTCCGGCGTTATTCTTGATGTCTCT
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 TCACCAGCAAAATCGCGCTGTAGCGGCCCATTAAGTTCTGTCTCGGCGCTGCGTCTGGCTGGCTGGCATAAATATC
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 CGAGTCCGGCTGCGGCTGGTGGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATATCCCGC
 CGTTAACCAACCATCAACAGGATTTTCGCCCTGCTGGGCAAAACAGCGTGGACCGTGTGCTGCAACTCTCTCAGGGCCAG
 GCGGTGAAGGGCAATCAGCTGTTCGCCGTCTCACTGGTGAAGAAACACACCCCTGGCGCCCAATACGCAACCGCCTC
 TCCCCGCGGTTGGCCGATTCAATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCA
 ATTAATGTAAGTTAGTCACTCACTATAGGCACCGGATCTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTT
 CCGGTGGCGCGGGCATGACTATCGTCGCCGCACTTATGACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGG
 CAGCGCTCTGGGTCAATTTCCGGCAGGACCGCTTTCGCTGGAGCGCGACGATGATCGGCCCTGTCGCTTGGGTATTCCGA
 ATCTTGACAGCCCTCGCTCAAGCCTTCGTCACCTGGTCCCGCCACCAACGTTTCGGCGAAGACAGGCCATTATCGCCGG
 CATGGCGGCCCCACGGGTGCGCATGATCGTCTCTGTGTTGAGGACCCGGCTAGGCTGGCGGGTTCGCTTACTGGTT
 AGCAGAAATGAATCACCGATACCGAGCGAAAGTGAAGCAGTCTGCTGCAAAACGCTGCGACCTGAGCAACAACATGA
 ATGGTCTTCGGTTTCGTTTCGTAAGTCTGGAACGCGGAAGTCAGCGCCCTGCACCATTATGTTCCGGATCTGCAT
 CGCAGGATGCTGCTGCCCTGTGGAACACCTACATCTGTATTAAACGAAGCGCTGGCATTGACCCCTGAGTGATTTTC
 TCTGGTCCCGCGCATCCATACCGCCAGTTGTTTACCCTCACAAAGTTCCAGTAACCGGCATGTTTCATCATCAGTAACC
 CGTATCGTGAGCATCTCTCTCGTTTCATCGGTATCATTAACCCCATGAACAGAAATCCCCCTTACACGGAGGCATCAGT
 GACCAACAGGAAACACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAAACGTTCTGGAGAACTCAACG
 AGCTGGACGGGATGAACAGGCAGACATCTGTGAATCGCTTACGACCAACGCTGATGAGCTTACCGCAGCTGCCCTCGCG
 CGTTTCGGTGATGACGGTGAACACCTCTGACACATGCAGCTCCCGAGACGGTACAGCTTGTCTGTAAAGCGGATGCCGG
 GAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCGCAGCCATGACCCAGTCACGTACGTAGCGATA
 GCGGAGTGTAATACTGGCTTAACATATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATATGCGGTGTGAAATACC
 GCACAGATGCGTAAGGAGAAATACCGCATCAGGCGCTCTTCGCTTCCCTCGTCACTGACTCGCTGCGTCGGTCGTTTC
 GGCTGCGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAAC
 ATGTGAGCAAAAGGCCAGCAACCGTAAAGGCCGCTGTGGCGTTTTCCTATAGGCTCCGCCCGCC
 TGACGAGCATCACAAATAACGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCC
 CTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCCCTGCGCGTTACCGGATACCTGTCCGCCCTTCTCCCTTCGGGAAGC
 GTGGCGCTTCTCATAGCTACGCTGAGGTATCTCAGTTTCGGTGTAGGTGTTTCGCTCCAAAGCTGGGCTGTGTGCACGA
 ACCCCCCGTTACGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCCGTAAGACACGACTTATCGC

Fig. 9A (continued)

CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
AACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAG
CTCTTGATCCGGCAAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATTACGCCGAGAAAAAAG
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ATGAACAATAAACTGTCTGCTTACATAAACAGTAATACAAAGGGTGTATGAGCCATATTCAACGGGAAACGTCCTTGCT
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GCGACAACTATCGATTGTATGGGAAGCCGATGCGCCAGAGTTGTTCTGAAACATGGCAAGGTAGCGTTGCCAATGA
TGTTACAGATGAGATGGTCAGACTAACTGGCTGACGGAAATTTATGCCTCTTCGACCATCAAGCATTTTATCCGTACTC
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TCGCGTATTTTCGCTCGCTCAGCGCAATCACGAATGAATAACGGTTTGGTTGATGCGAGTGATTTTGATGACGAGCGTA
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GATTTCTCACTTGATAACCTTATTTTGGACGAGGGGAAATTAATAGGTTGTATTGATGTTGGACGAGTCGGAATCGCAGA
CCGATACCAGGATCTTGCCATCCTATGGAACCTGCCTCGGTGAGTTTCTCCTTCATTACAGAAACGGCTTTTTCAAAAAT
ATGGTATTGATAATCCTGATATGAATAAATTGCAGTTTCAATTTGATGCTCGATGAGTTTTTCTAAGAAATTAATTCATGAG
CGGATACATAATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGAATC
TTGTAAACGGTTAATATTTTGTAAATTCGCGTTAAATTTTGTAAATCAGCTCATTTTTTTAACCAATAGGCCGAAATC
GGCAAAATCCCTTAATAATCAAAAGAAATAGACCGAGATAGGGTTGAGTGTTCAGTTTGGACACAAGATCCACTATT
AAAGAACGTGGACTCCAACGTCAAAGGGGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAAT
CAAGTTTTTTGGGGTCGAGGTGCCGTAAGCACTAAATCGGAACCTTAAGGGAGCCCCCGATTAGAGCTTGACGGGGA
AAGCCGGCAACGTGGCGAGAAAGGAAGGAAAGCAAGGAGCGGCGCTAGGGCGCTGGCAAGGTAGCGGTAC
GCTGCGCGTAACCAACACACCCGCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCA

Fig. 9A (continued)

Figure 9B

(SEQ ID No.:41)

MGIEEGKLVINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEI
TPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLLYNKDLLPNPPKTWEELPALDKELKAKGKSALMFNLQEPYFTWP
LIAADGGYAFKYENKGYDIKDVGVNAGAKAGLTFVLVDLIKKNHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSK
VNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAA
TMENAQKEIMPNIQMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSSGSGSGMDEKTTGWRGGHVVEGLAGELEQ
LRARLEHHPQGQREPGSGHHHHHEF

Fig. 9B

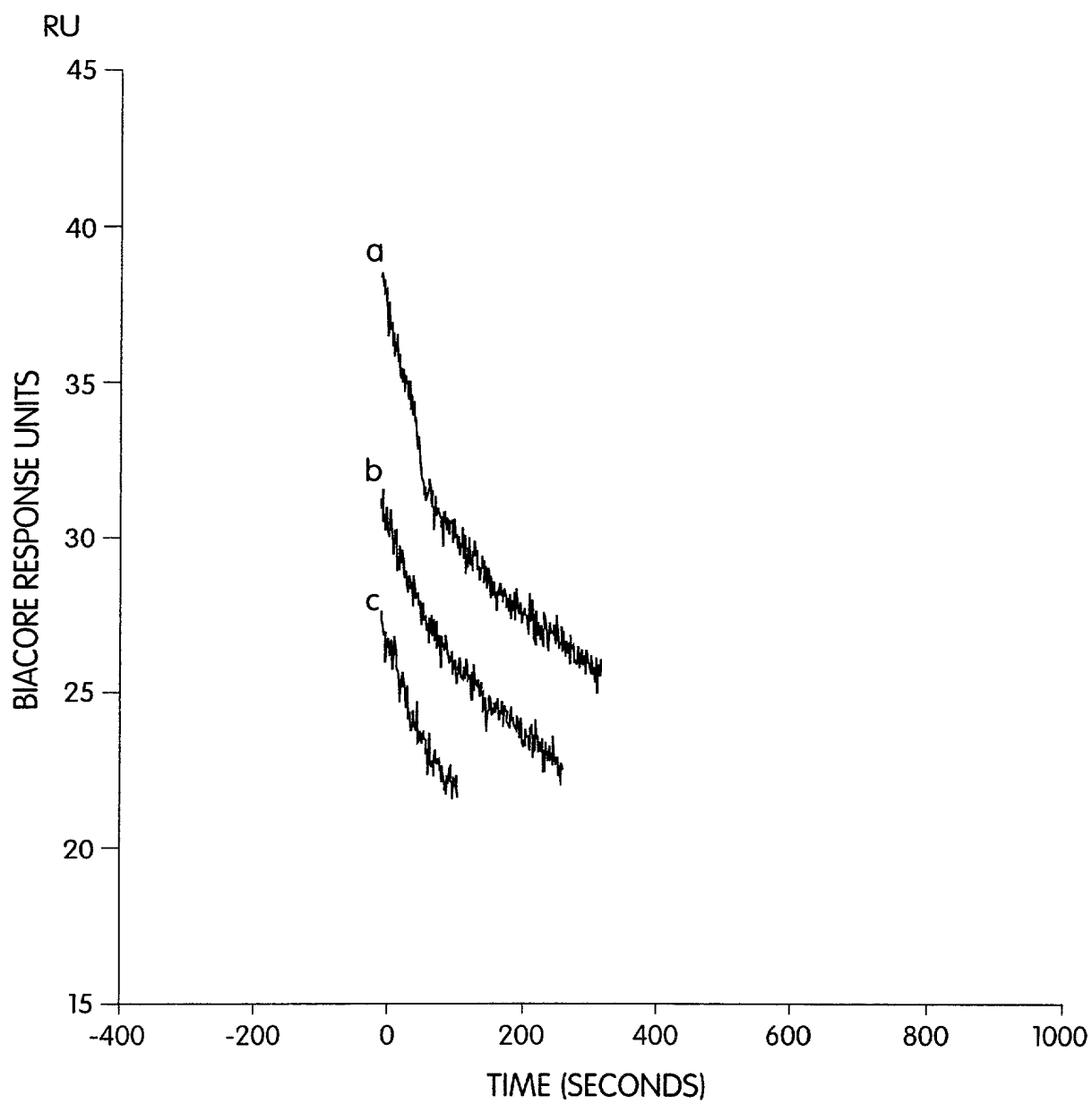


Fig. 10A

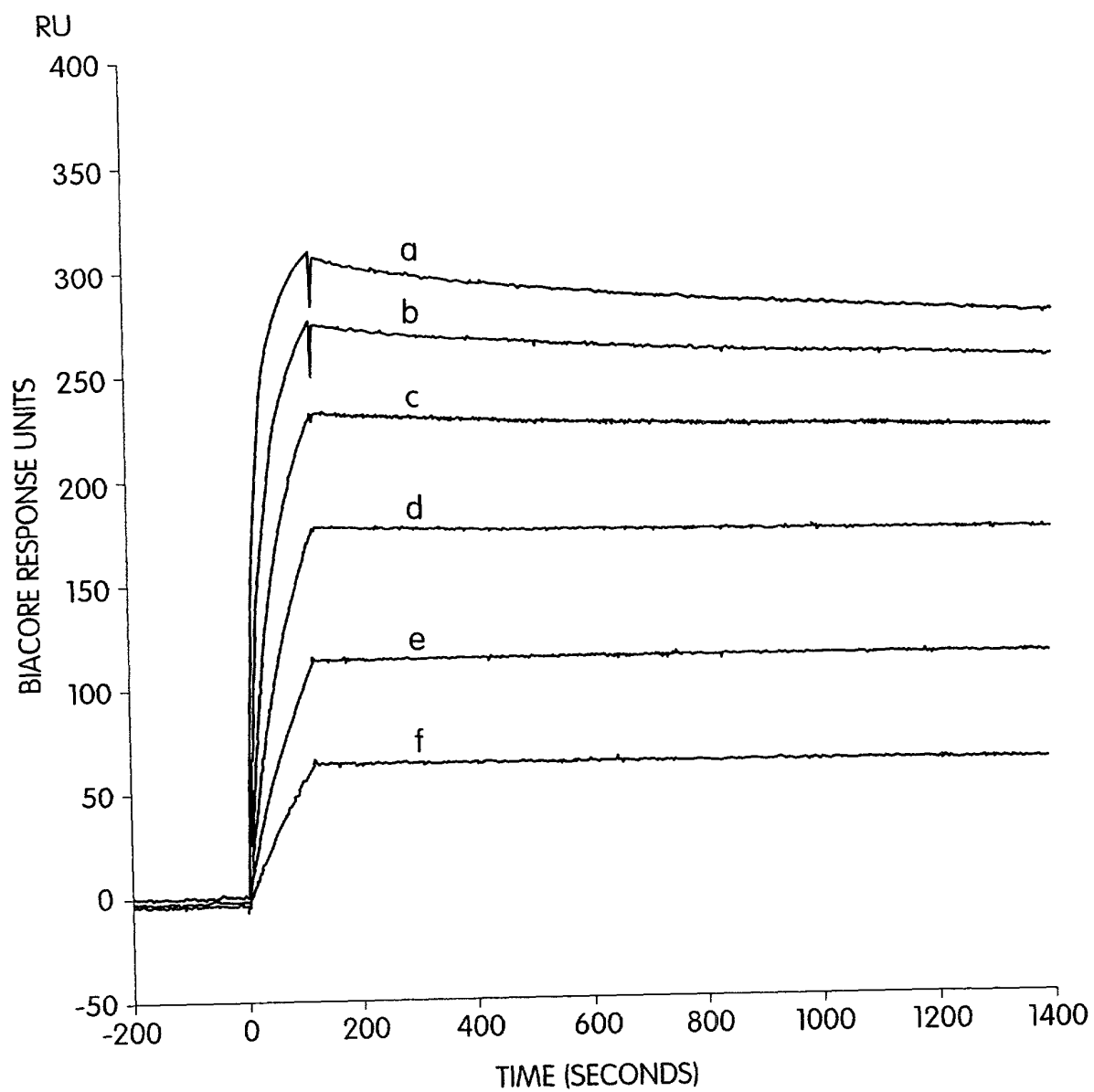


Fig. 10B

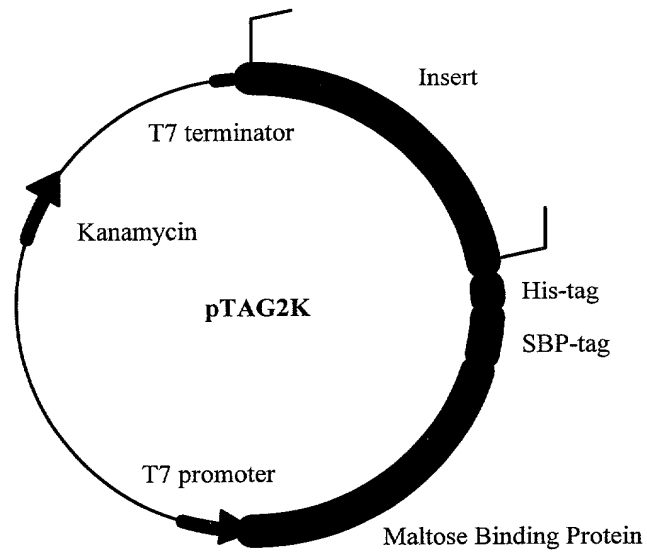


Fig. 11

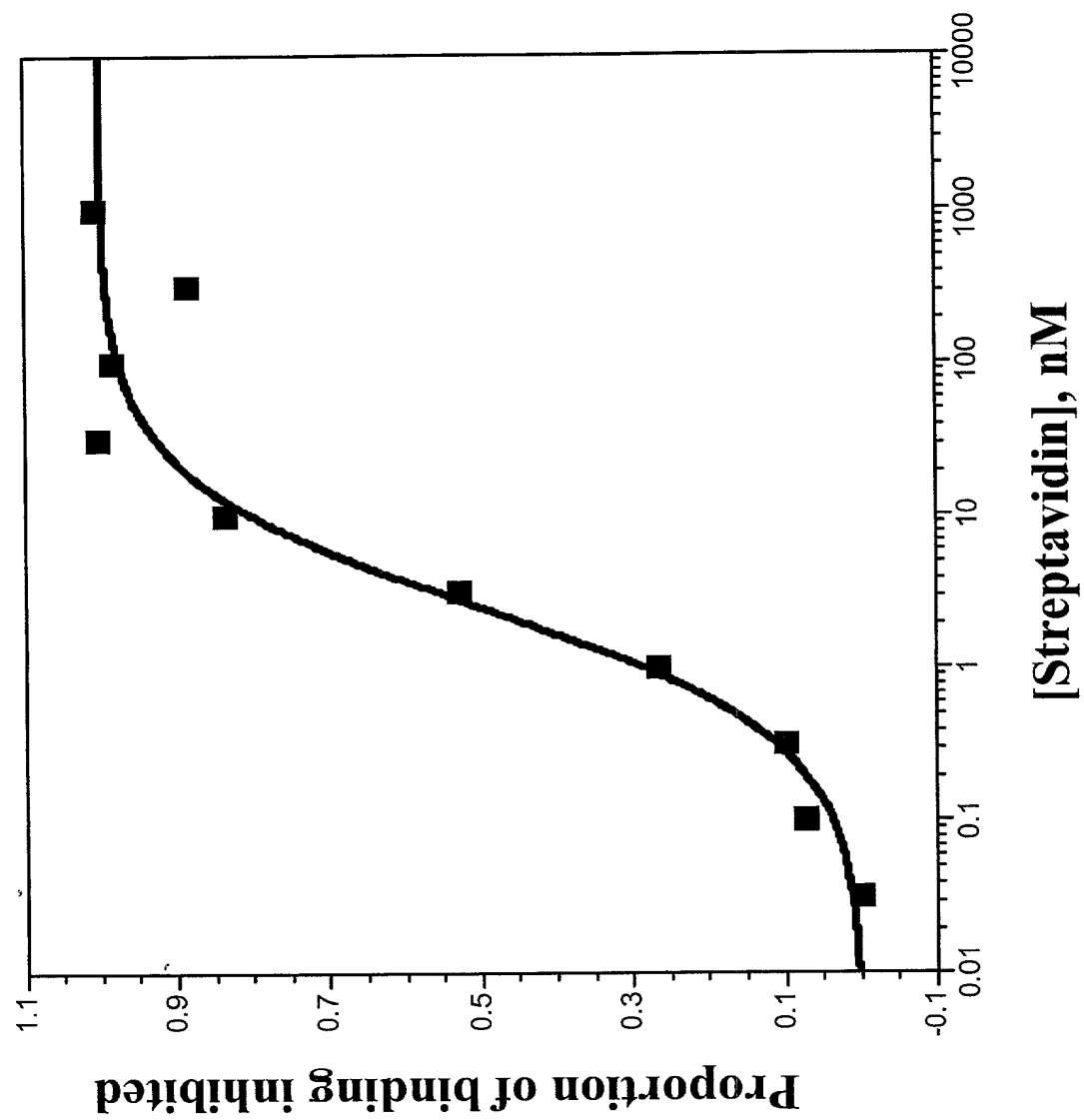


Fig. 12

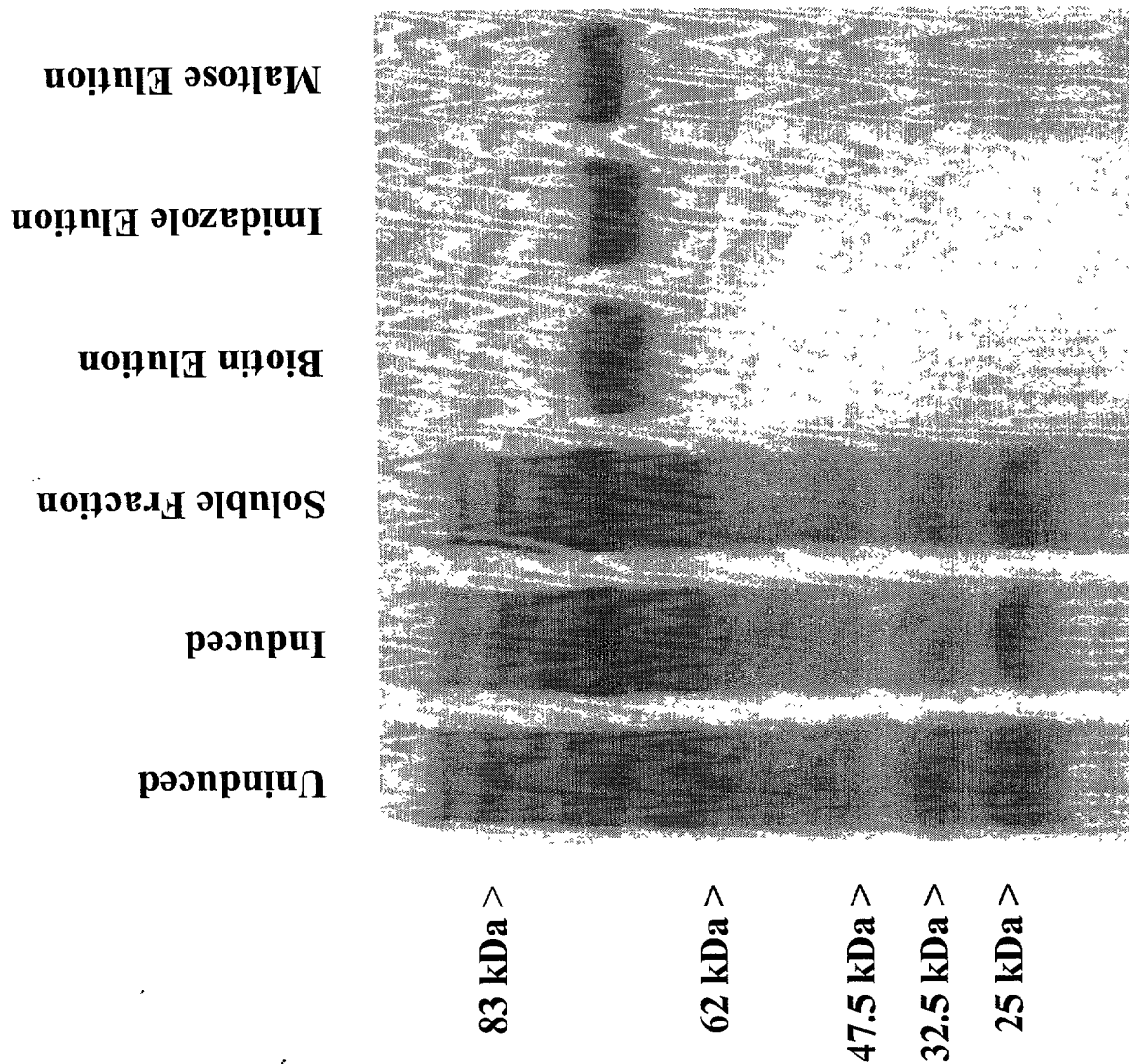
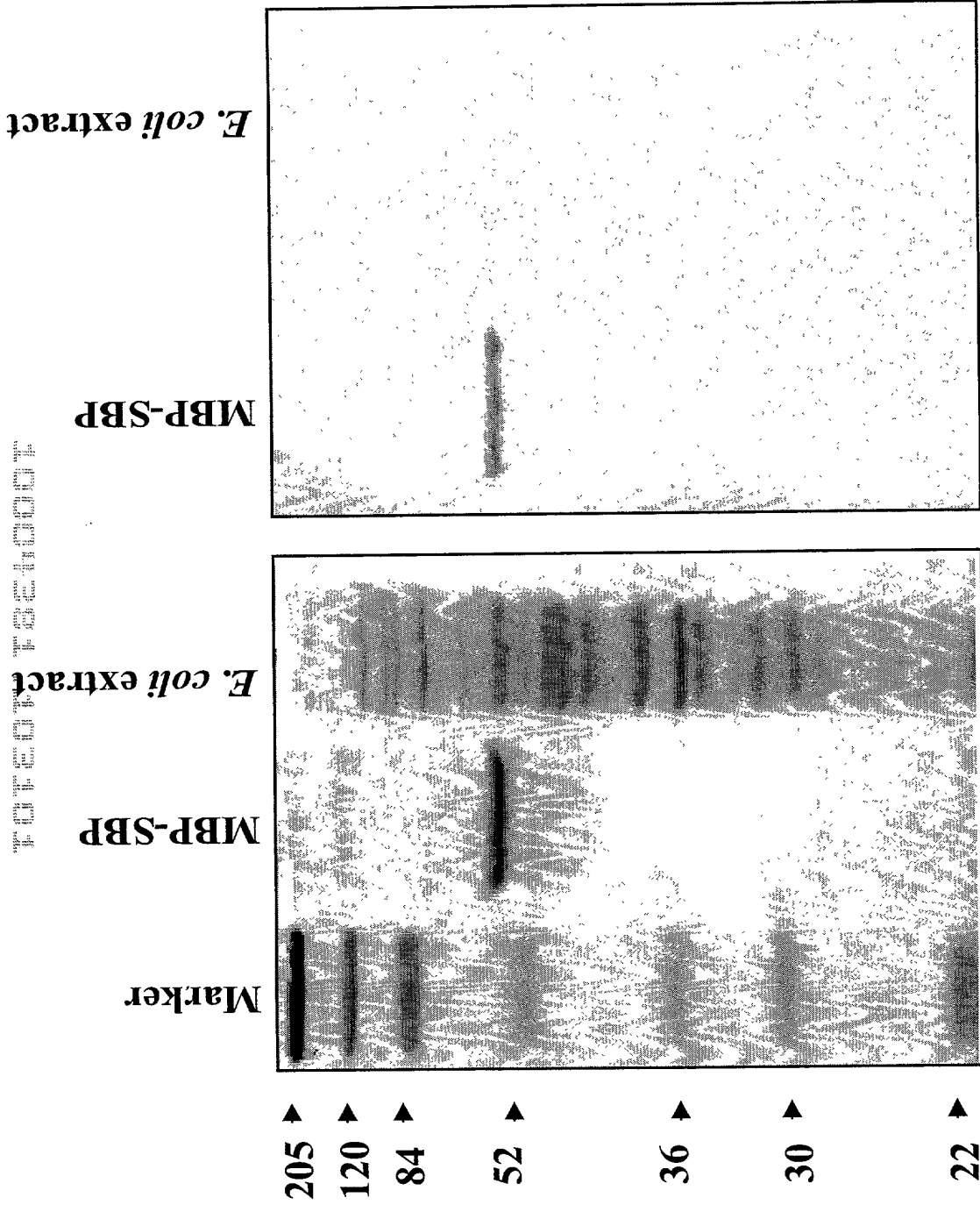


Fig. 13



Blot developed with SA-HRP

Total protein stain

Fig. 14

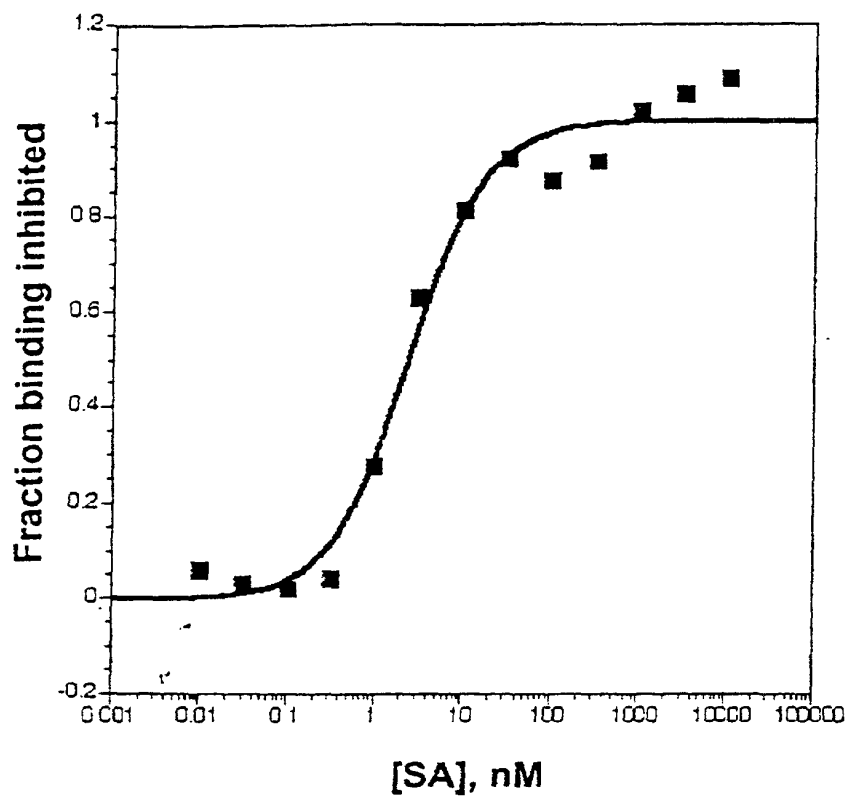


Fig. 15